Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:02:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472509.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3472509 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472509_1.fastq.gz SRR3472509_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:02:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472509.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,447,514
Mapped reads	16,229,773 / 98.68%
Unmapped reads	217,741 / 1.32%
Mapped paired reads	16,229,773 / 98.68%
Mapped reads, first in pair	8,143,190 / 49.51%
Mapped reads, second in pair	8,086,583 / 49.17%
Mapped reads, both in pair	16,118,900 / 98%
Mapped reads, singletons	110,873 / 0.67%
Secondary alignments	0
Supplementary alignments	55,688 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	9,999,205 / 60.79%
Duplication rate	44.83%
Clipped reads	1,298,358 / 7.89%

2.2. ACGT Content

Number/percentage of A's	442,708,287 / 27.72%
Number/percentage of C's	358,185,327 / 22.43%
Number/percentage of T's	440,421,360 / 27.57%
Number/percentage of G's	355,668,949 / 22.27%
Number/percentage of N's	247,556 / 0.02%

GC Percentage	44.69%

2.3. Coverage

Mean	0.516
Standard Deviation	17.7505

2.4. Mapping Quality

Mean Mapping Quality	55.02

2.5. Insert size

Mean	25,974.01
Standard Deviation	1,596,828.46
P25/Median/P75	175 / 247 / 336

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,071,632
Insertions	87,789
Mapped reads with at least one insertion	0.53%
Deletions	79,264
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.72%

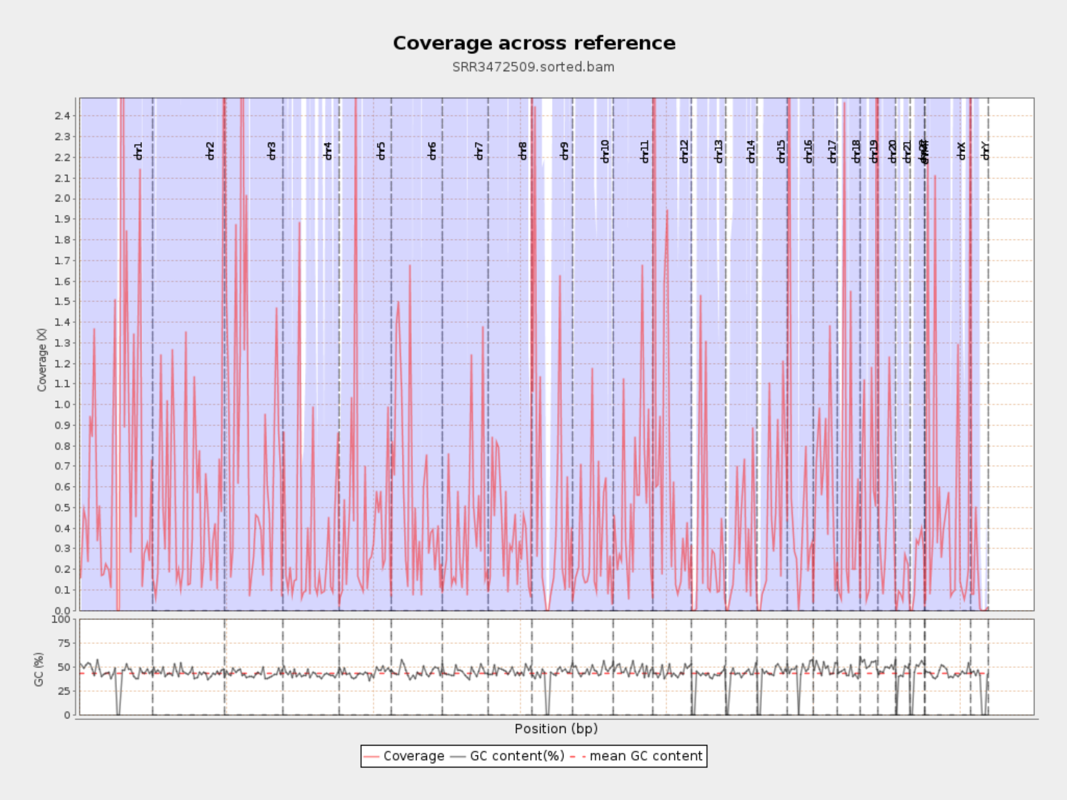
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

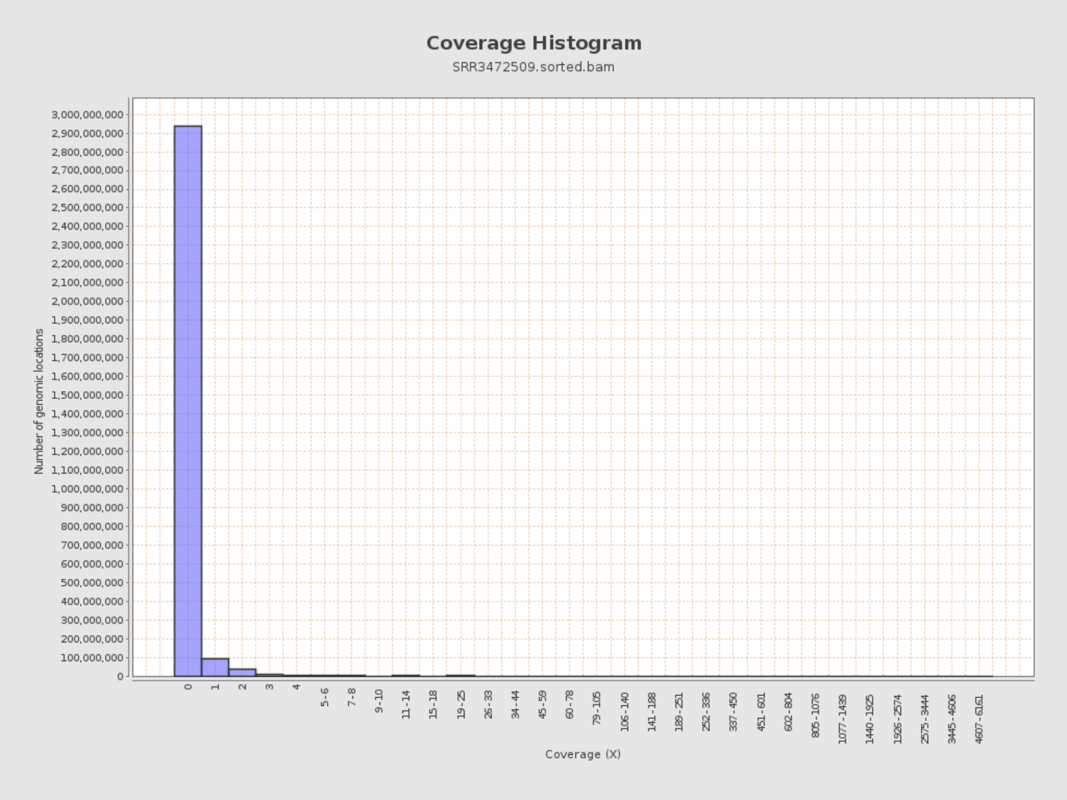
		bases	coverage	deviation
chr1	249250621	187853488	0.7537	24.0737
chr2	243199373	124524571	0.512	18.6205
chr3	198022430	177154522	0.8946	23.4924
chr4	191154276	60913257	0.3187	10.4992
chr5	180915260	83747267	0.4629	15.1209
chr6	171115067	94015707	0.5494	14.6
chr7	159138663	64779028	0.4071	13.5957
chr8	146364022	55730087	0.3808	11.7463
chr9	141213431	77249948	0.547	14.9956
chr10	135534747	43840319	0.3235	13.2922
chr11	135006516	74073130	0.5487	20.1399
chr12	133851895	105794915	0.7904	27.8992
chr13	115169878	41364205	0.3592	12.6536
chr14	107349540	33159996	0.3089	10.5056
chr15	102531392	46884582	0.4573	16.3604
chr16	90354753	50992803	0.5644	15.6101
chr17	81195210	51550316	0.6349	13.411
chr18	78077248	44563958	0.5708	33.1119
chr19	59128983	42930305	0.726	25.3156
chr20	63025520	30917543	0.4906	13.5655
chr21	48129895	5881245	0.1222	4.8827
chr22	51304566	11162486	0.2176	5.1672
chrMT	16571	2389	0.1442	0.5606
chrX	155270560	81623687	0.5257	16.2771

chrY	59373566	6720584	0.1132	4.0152

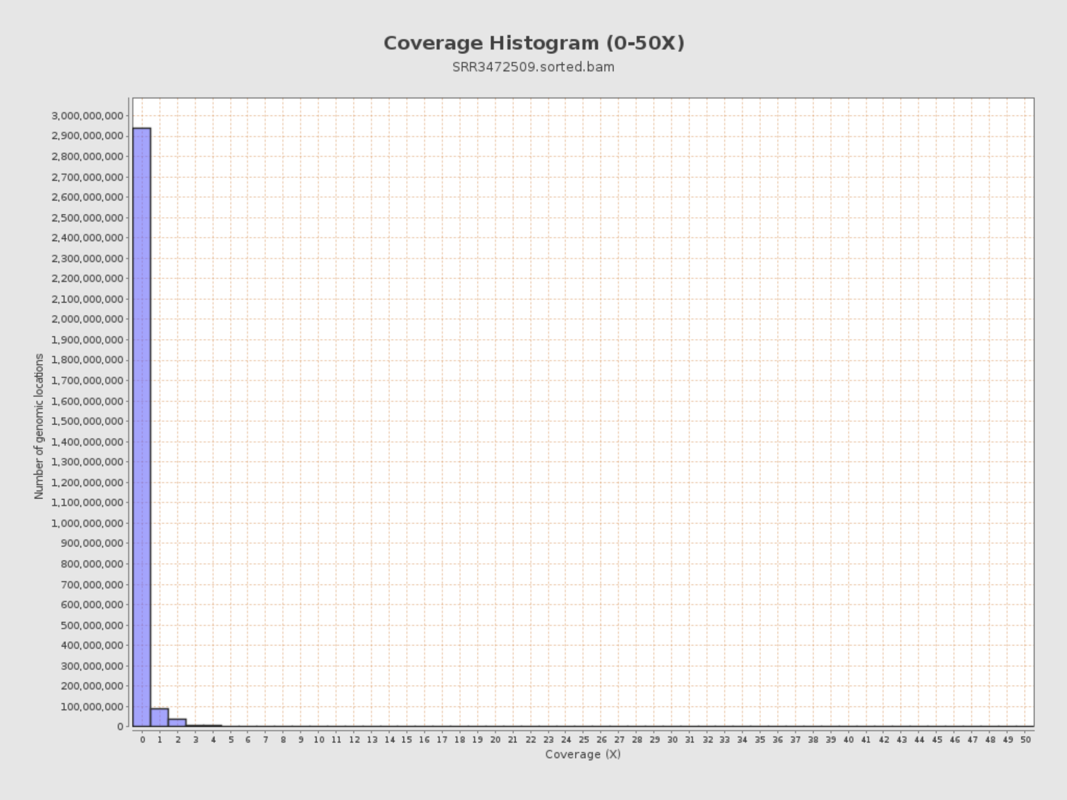
3. Results : Coverage across reference



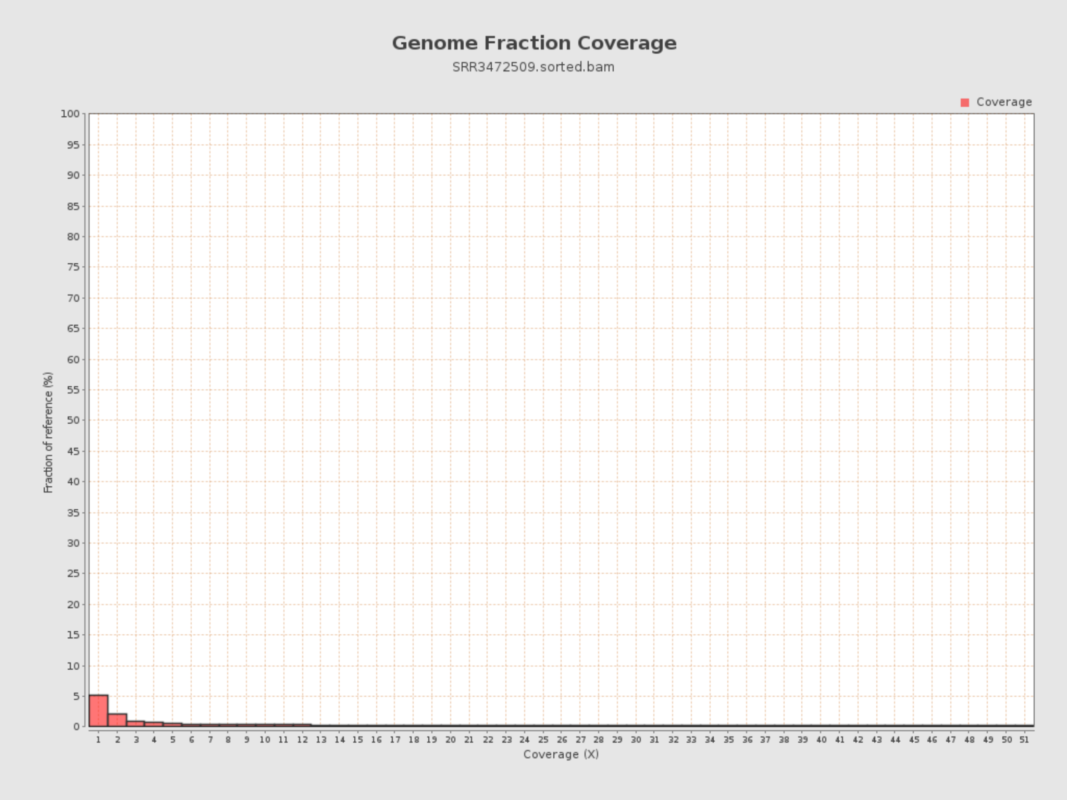
4. Results : Coverage Histogram



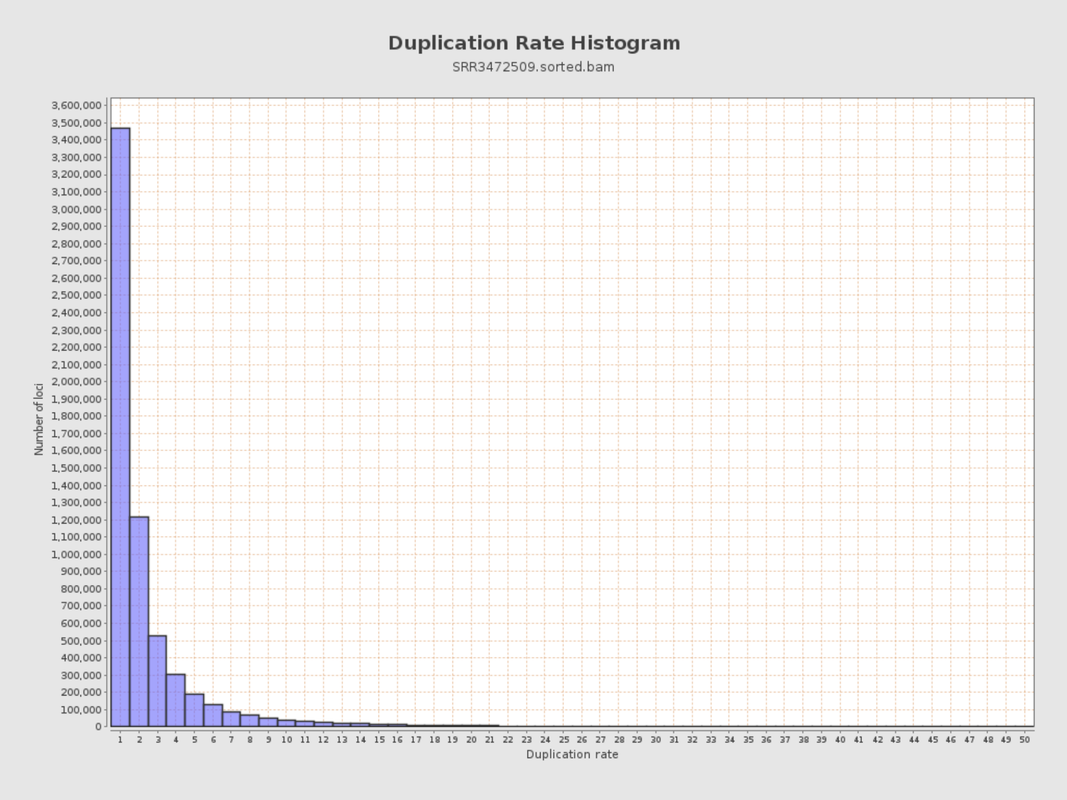
5. Results : Coverage Histogram (0-50X)



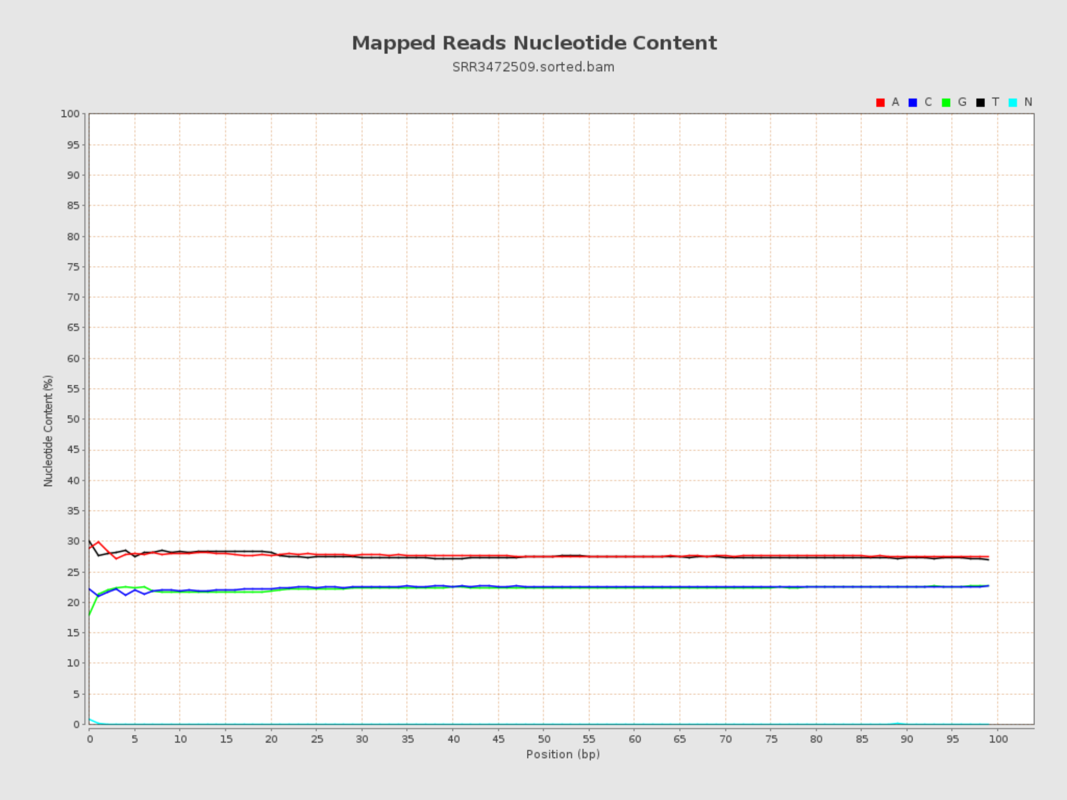
6. Results : Genome Fraction Coverage



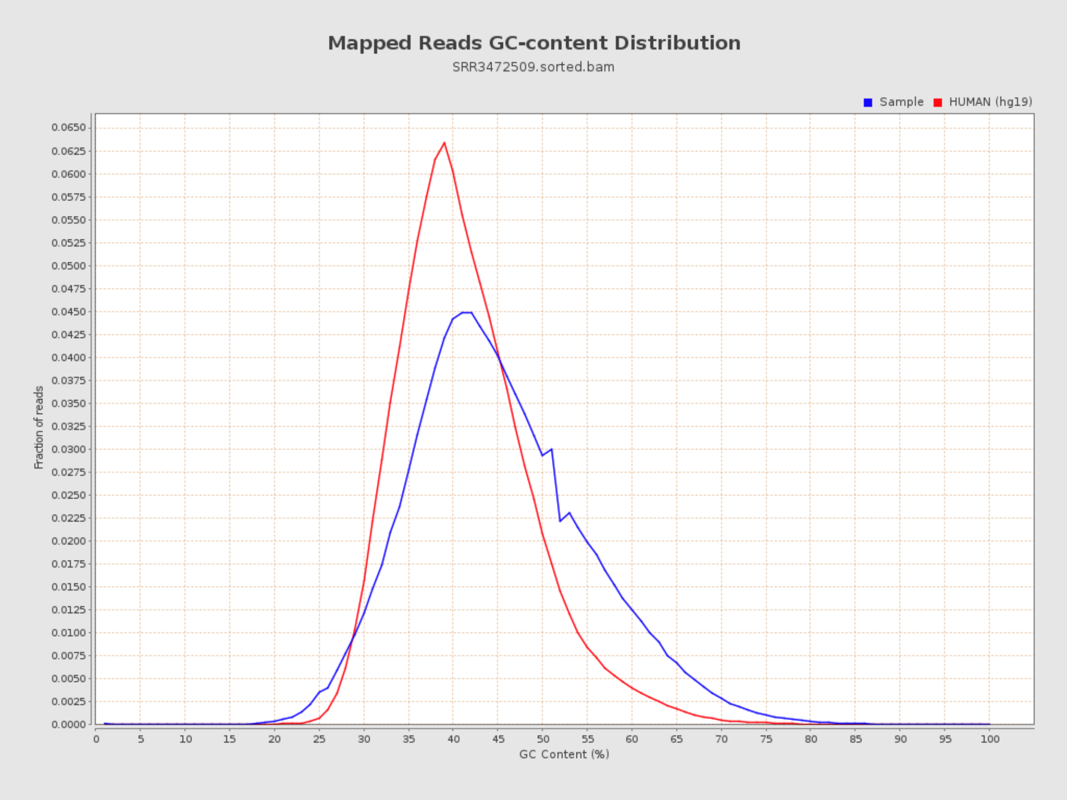
7. Results : Duplication Rate Histogram



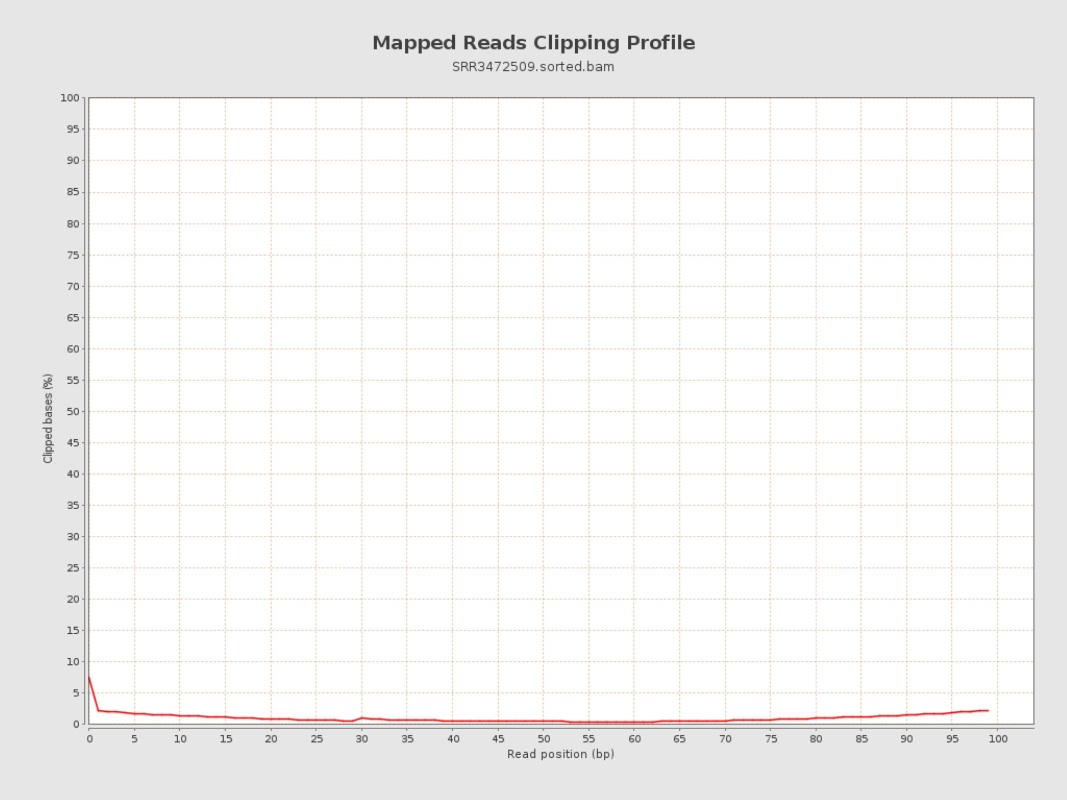
8. Results : Mapped Reads Nucleotide Content



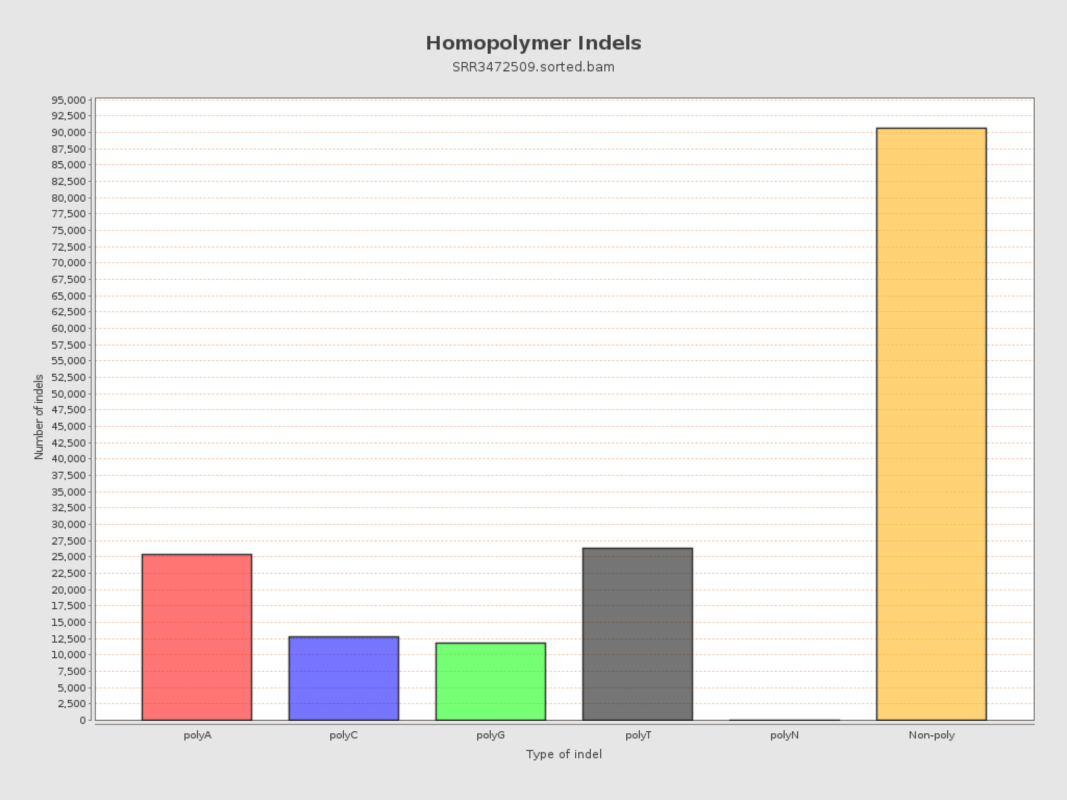
9. Results : Mapped Reads GC-content Distribution



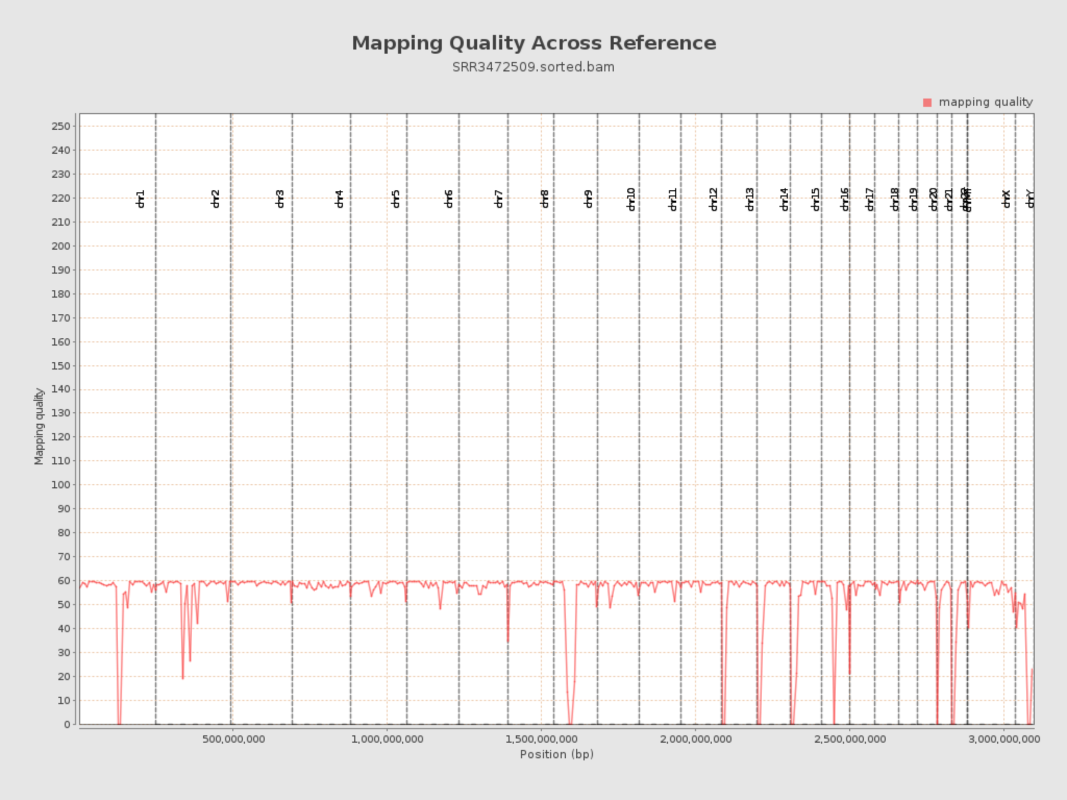
10. Results : Mapped Reads Clipping Profile



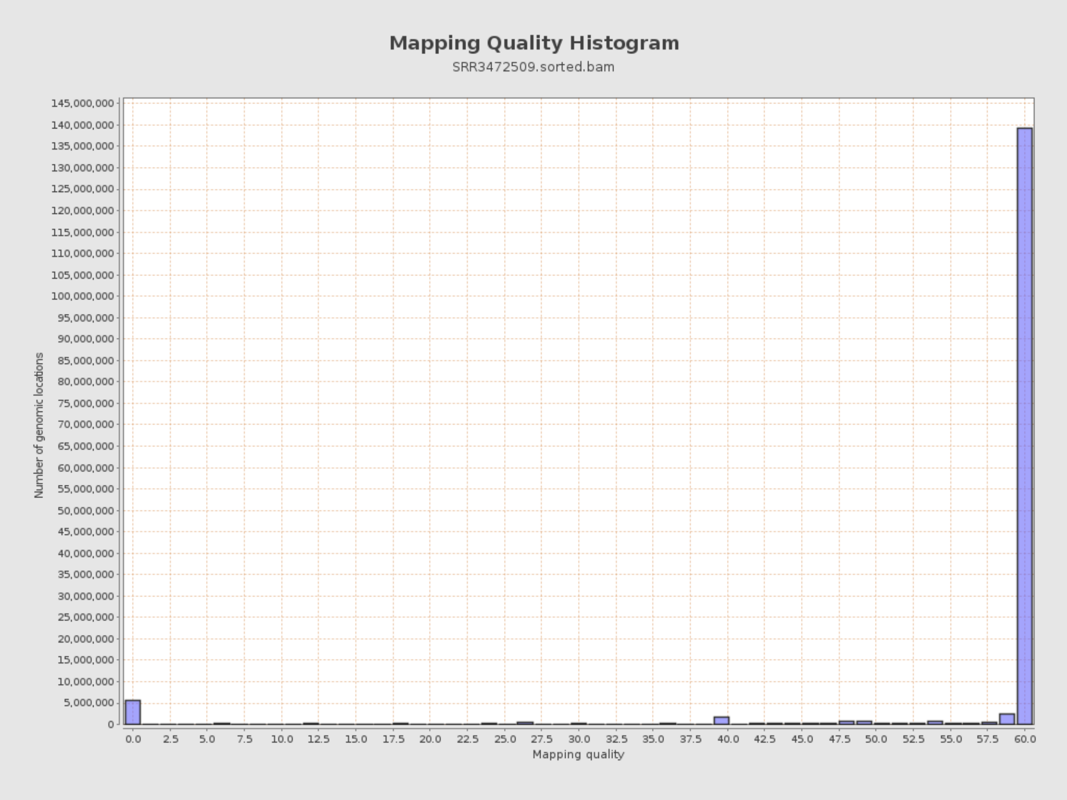
11. Results : Homopolymer Indels



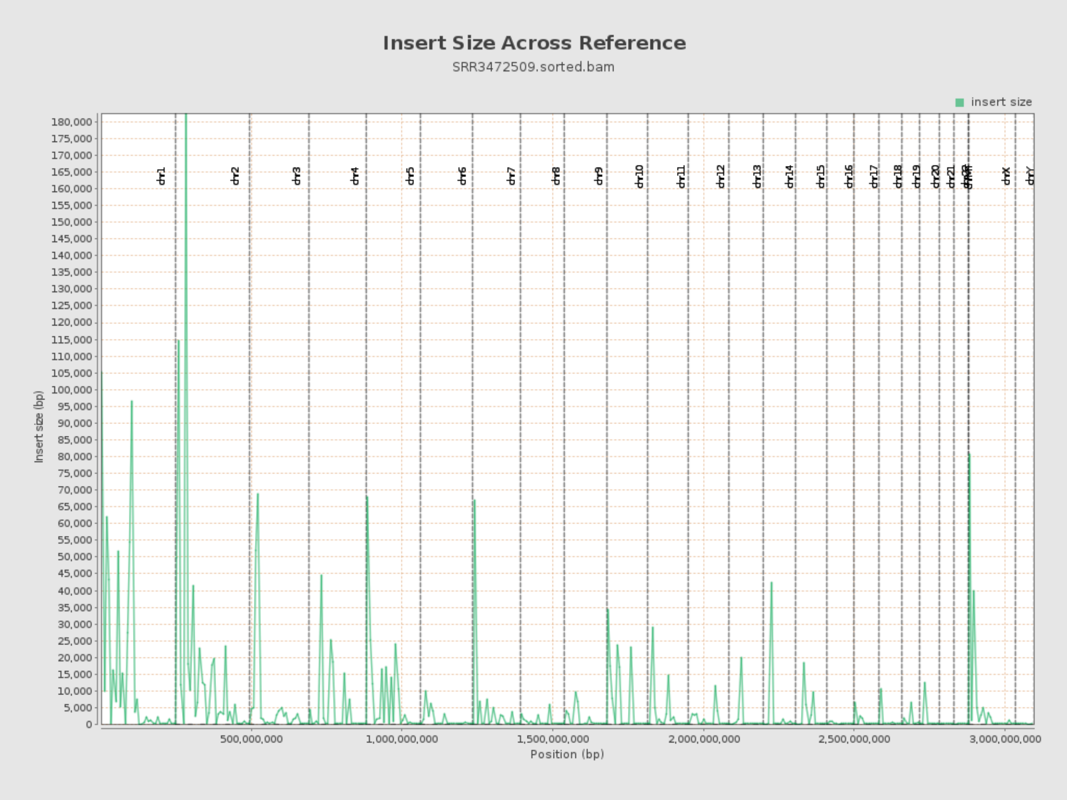
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram